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OM nucleic - nucleic search, using sw model

Run on: March 7, 2003, 11:36:59 : Search time 168 Seconds
(without alignments)
768.323 Million cell updates/sec

Title: US-09-220-617B-203

Perfect score: 471

Sequence: 1 ATGCCCTAGGGAGTTCCT.....CCTGGGGTGGTGGTGA 471

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15333381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : Issued_Patents_NA*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	471	100.0	471	4 US-08-931-858E-203	Sequence 203, App
c 2	471	100.0	471	4 US-08-931-858E-204	Sequence 204, App
c 3	467.8	99.3	471	4 US-08-931-858E-205	Sequence 205, App
c 4	467.8	99.3	471	4 US-08-931-858E-206	Sequence 206, App
c 6	291	61.8	291	4 US-08-931-858E-199	Sequence 199, App
c 7	289.4	61.4	291	4 US-08-931-858E-200	Sequence 200, App
c 8	289.4	61.4	291	4 US-08-931-858E-201	Sequence 201, App
c 9	267	56.7	267	4 US-08-931-858E-222	Sequence 222, App
c 10	250	53.1	471	4 US-08-931-858E-179	Sequence 179, App
c 11	250	53.1	471	4 US-08-931-858E-180	Sequence 180, App
c 12	250	53.1	471	4 US-08-931-858E-190	Sequence 190, App
c 13	250	53.1	471	4 US-08-931-858E-191	Sequence 191, App
c 14	207.6	44.1	405	4 US-08-931-739-175	Sequence 175, App
c 15	207.6	44.1	405	4 US-09-128-026-131	Sequence 131, App
c 16	207.6	44.1	544	4 US-08-931-858E-105	Sequence 131, App
c 17	207.6	44.1	544	4 US-08-981-739-105	Sequence 105, App
c 18	207.6	44.1	544	4 US-09-128-026-105	Sequence 105, App
c 19	207.6	44.1	559	4 US-08-931-858E-131	Sequence 131, App
c 20	207.6	44.1	559	4 US-08-981-739-131	Sequence 131, App
c 21	207.6	44.1	559	4 US-09-128-026-131	Sequence 131, App
c 22	207.6	44.1	723	4 US-08-931-858E-177	Sequence 178, App
c 23	207.6	44.1	723	4 US-08-931-858E-178	Sequence 188, App
c 24	203	43.1	559	4 US-08-931-858E-188	Sequence 188, App
c 25	203	43.1	559	4 US-08-931-858E-189	Sequence 189, App
c 26	203	43.1	559	4 US-08-981-739-134	Sequence 134, App
c 27	203	43.1	559	4 US-09-128-026-134	Sequence 134, App

ALIGNMENTS

RESULT 1
US-08-931-858E-203
; Sequence 203, Application US/08931858E
; Patent No. 622022
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, EUGENE M
; APPLICANT: MILBRANDT, JEFFREY D
; APPLICANT: KOPZBAUER, PAUL T
; APPLICANT: LAMPE, PATRICIA A
; APPLICANT: KLEIN, ROBERT
; APPLICANT: DESAUVAGE, FRED
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESS: HOWELL & HAERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931-858E
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 971486
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08 931-858E-203

Query Match Length DB ID Description

Sequence 203, App

Sequence 204, App

Sequence 205, App

Sequence 206, App

Sequence 199, App

Sequence 200, App

Sequence 201, App

Sequence 222, App

Sequence 179, App

Sequence 180, App

Sequence 190, App

Sequence 191, App

Sequence 175, App

Sequence 175, App

Sequence 105, App

Sequence 105, App

Sequence 105, App

Sequence 131, App

Sequence 131, App

Sequence 178, App

Sequence 188, App

Sequence 189, App

Sequence 134, App

Score 471; DB 4; Length 471;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCCCTAGGGAGTTCCTGGGGCTCTCTGCTGAGCTGGACAG 60

REFERENCE/DOCKET NUMBER: 971486
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 314-727-5188
 TELEFAX: 314-727-6092
 INFORMATION FOR SEQ ID NO: 205:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 471 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-931-858E-205

Query Match Similarity 99.3%; Score 467.8; DB 4; Length 471;
 Matches 469; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 ATGGCGTAGGAAGTGGCTCGCTGGCTCTGGTGCAGCTGGGACAG 60
 Db 1 ATGGCCCTAGGAAAGTCCCTGGCTCCCTGGCTCTGGTGCAGCTGGGACAG 60
 Qy 61 GGCGGGCCGGATGCCCTGGGTTCGGTGCATGGAGAGTCTCGTCTGAAAG 120
 Db 61 GGCGGGCCGGATGCCCTGGGTTCGGTGCATGGAGAGTCTCGTCTGAAAG 120
 Qy 121 GTCGAAAGGCTGGAGGACCTGGTGGCACCCACCCCTTGGCGCCTGGCGA 180
 Db 121 GTCGAAAGGCTGGAGGACCTGGTGGCACCCACCCCTTGGCGCCTGGCGA 180
 Qy 181 GGCCTGCTGGTCATGCCAGCTGTGGACGACTGGCCCTGGCGACCTGGCG 240
 Db 181 GGCCTGCTGGTCATGCCAGCTGTGGACGACTGGCCCTGGCGACCTGGCG 240
 Qy 241 GGCCTACGCTAGAGGAGGTCTCTTCCGCTACTCGGGGCAACTGCCCGCTGGT 300
 Db 241 GGCCTACGCTAGAGGAGGTCTCTTCCGCTACTCGGGGCAACTGCCCGCTGGT 300
 Qy 301 GCGGACCCAGCATGGCTGGCTGGCCGACTGGGGCCAGGCCACGGT 360
 Db 301 GCGGACCCAGCATGGCTGGCTGGCCGACTGGGGCCAGGCCACGGT 360
 Qy 361 GGCGCTGGCTGGCCACTCGTACACCCAGCTGGCTGGCCGACTGGGGCCAGGCCACGGC 420
 Db 361 GGCGCTGGCTGGCCGACTCGTACACCCAGCTGGCTGGCCGACTGGGGCCAGGCCACGGC 420
 Qy 421 TGGCAAGGGGCCCCAGCTCGGGCTGGCTGGGGCTGGCTGGCTGA 471
 Db 421 TGGAGGGCTGGCTGGCTGGGGCTGGCTGGGGCTGGCTGGCTGA 471

RESULT 4
 US-08-931-858E-206/c
 Sequence 206, Application US/08931858E
 Patent No. 6222022
 GENERAL INFORMATION:
 ADDRESSEE: HOWELL S. HAERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MO
 COUNTRY: USA
 ZIP: 63105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
 NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESS:
 APPLICANT: JOHNSON, EUGENE M
 APPLICANT: MILBRANDT, JEFFREY D
 APPLICANT: KOTZBAUER, PAUL T
 APPLICANT: LAMPE, PATRICIA A
 APPLICANT: KLEIN, ROBERT
 APPLICANT: DESAUVAGE, FRED

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/931,858E
 FILING DATE: 4/35
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 971486
 TELEPHONE: 314-727-5188
 TELECOMMUNICATION INFORMATION:
 INFORMATION FOR SEQ ID NO: 206:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 471 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-931-858E-206

Query Match Similarity 99.3%; Score 467.8; DB 4; Length 471;
 Best Local Similarity 99.3%; Pred. No. 8.3e-90;
 Matches 469; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 ATGGCGTAGGAAGTGGCTCGCTGGCCTCTGGCAGCTGGGACAG 60
 Db 471 ATGGCGTAGGAAGTGGCTCGCTGGCCTCTGGCAGCTGGGACAG 412
 Qy 61 GGCGGGCCGGATGCCCTGGGTTCGGTGCATGGAGAGTCTCGTCTGAAAG 120
 Db 411 GGCGGGCCGGATGCCCTGGGTTCGGTGCATGGAGAGTCTCGTCTGAAAG 352
 Qy 121 GTCGAAAGGCTGGAGGACCTGGTGGCACCCACCCCTTGGCGCCTGGCGA 180
 Db 121 GTCGAAAGGCTGGAGGACCTGGTGGCACCCACCCCTTGGCGCCTGGCGA 180
 Qy 181 GGCCTGCTGGTCATGCCAGCTGTGGACGACTGGCCCTGGCGACCTGGCG 240
 Db 181 GGCCTGCTGGTCATGCCAGCTGTGGACGACTGGCCCTGGCGACCTGGCG 240
 Qy 241 GGCCTACGCTAGAGGAGGTCTCTTCCGCTACTCGGGGCAACTGCCCGCTGGT 300
 Db 241 GGCCTACGCTAGAGGAGGTCTCTTCCGCTACTCGGGGCAACTGCCCGCTGGT 300
 Qy 301 GCGGACCCAGCATGGCTGGCTGGCCGACTGGGGCCAGGCCACGGT 360
 Db 301 GCGGACCCAGCATGGCTGGCTGGCCGACTGGGGCCAGGCCACGGT 360
 Qy 361 GGCGCTGGCTGGCCACTCGTACACCCAGCTGGCTGGCCGACTGGGGCCAGGCCACGGC 420
 Db 361 GGCGCTGGCTGGCCGACTCGTACACCCAGCTGGCTGGCCGACTGGGGCCAGGCCACGGC 420
 Qy 421 TGGCAAGGGGCCCCAGCTCGGGCTGGGGCTGGCTGGCTGA 471
 Db 421 TGGAGGGCTGGCTGGGGCTGGGGCTGGCTGGCTGA 471

RESULT 5
 US-08-931-858E-199
 Sequence 199, Application US/08931858E
 Patent No. 6222022
 GENERAL INFORMATION:
 APPLICANT: JOHNSON, EUGENE M
 APPLICANT: MILBRANDT, JEFFREY D
 APPLICANT: KOTZBAUER, PAUL T
 APPLICANT: LAMPE, PATRICIA A
 APPLICANT: KLEIN, ROBERT
 APPLICANT: DESAUVAGE, FRED
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
 NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL, & HAERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MO
 COUNTRY: USA
 ZIP: 63105

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/931,858E
 FILING DATE: US-08-931-858E-200

CLASSIFICATION: 415
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 971486
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 314-727-5188
 TELEFAX: 314-727-6092
 INFORMATION FOR SEQ ID NO: 199:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 291 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-931-858E-199

Query Match 61.8%; Score 291; DB 4; Length 291;
 Best Local Similarity 100.0%; Pred. No. 7e-53; 0; Mismatches 0; Indels 0; Gaps 0;

Match 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 181 GCGCTTCGTCATGGCCAGCTGGCCCTGCGCTGGCCAGCTAGGCCCTG 240
 Db 1 GCGCTTCGTCATGGCCAGCTGGCCCTGCGCTGGCCAGCTAGGCCCTG 60
 Qy 241 GCGTACCCCTAGAGAGGGTCACTTCGGCTACGGCGGGGAGCTGGCCCTG 300
 Db 61 GCGTAGCCCTAGAGAGGGTCACTTCGGCTACGGCGGGGAGCTGGCCCTG 120
 Qy 301 GCGCCGACCCAGCTGGCCCTGGCCGCTGGCCGAGGCCAACGGT 360
 Db 121 GCGCGACCCAGCTGGCCCTGGCCGCTGGCCGAGGCCAACGGT 180
 Qy 361 GGGCCCTGCGCCGCTGGCCGCTGGCCGCTGGCCGCTGGCCGCTGGCC 420
 Db 181 GGGCCCTGCGCCGCTGGCCGCTGGCCGCTGGCCGCTGGCCGCTGGCC 240
 Qy 421 TGGCAAGGGCTGGCCAGCTCGGGGCTGGCCAGCTGGCCGCTGGCC 471
 Db 241 TGGCAAGGGCTGGCCAGCTCGGGGCTGGCCAGCTGGCCGCTGGCC 291

RESULT 6
 US-08-931-858E-200/C
 Sequence 200, Application US/08931858E
 Patent No. 6222022

GENERAL INFORMATION:
 APPLICANT: JOHNSON, EUGENE M
 APPLICANT: MILBRANDT, JEFFREY D
 APPLICANT: KOTZBAUER, PAUL T
 APPLICANT: LAMPE, PATRICIA A
 APPLICANT: KLEIN, ROBERT
 APPLICANT: DESAUVAGE, FRED
 APPLICANT: KLEIN, ROBERT
 APPLICANT: DESAUVAGE, FRED
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
 NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL, & HAERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MO
 COUNTRY: USA
 ZIP: 63105

STATE: MO
 COUNTRY: USA
 ZIP: 63105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/931,858E
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 971486
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 314-727-5188
 TELEFAX: 314-727-6092
 INFORMATION FOR SEQ ID NO: 200:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 291 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-931-858E-200

Query Match 61.8%; Score 291; DB 4; Length 291;
 Best Local Similarity 100.0%; Pred. No. 7e-53; 0; Mismatches 0; Indels 0; Gaps 0;

Match 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 181 GCGCTTCGTCATGGCCAGCTGGCCCTGCGCTGGCCAGCTAGGCCCTG 240
 Db 291 GCGCTTCGTCATGGCCAGCTGGCCCTGCGCTGGCCAGCTAGGCCCTG 232
 Qy 241 GGCTAGCCCTAGAGAGGGTCACTTCGGCTACGGCGGGAGCTGGCCCTG 300
 Db 231 GGCTAGCCCTAGAGAGGGTCACTTCGGCTACGGCGGGAGCTGGCCCTG 172
 Qy 301 GCGCAGCCAGATGGCTGGCCCTGGCCAGCTGGCCCTGGCCAGCTGGCT 360
 Db 171 GCGCCGACCCAGCTGGCCCTGGCCCTGGCCCTGGCCAGGGCCACGGT 112
 Qy 361 GGGCCCTGCGCCGCTGGCCGCTGGCCGCTGGCCGCTGGCCGCTGGCC 420
 Db 111 GGGCCCTGCGCCGCTGGCCGCTGGCCGCTGGCCGCTGGCCGCTGGCC 52
 Qy 421 TGGCAAGGGCTGGCCAGCTCGGGGCTGGCCAGCTGGCCGCTGGCC 471
 Db 51 TGGCAAGGGCTGGCCAGCTCGGGCTGGCCAGCTGGCCGCTGGCC 1

RESULT 7
 US-08-931-858E-201
 Sequence 201, Application US/08931858E
 Patent No. 6222022

GENERAL INFORMATION:
 APPLICANT: JOHNSON, EUGENE M
 APPLICANT: MILBRANDT, JEFFREY D
 APPLICANT: KOTZBAUER, PAUL T
 APPLICANT: LAMPE, PATRICIA A
 APPLICANT: KLEIN, ROBERT
 APPLICANT: DESAUVAGE, FRED
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
 NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL, & HAERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MO
 COUNTRY: USA
 ZIP: 63105

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/931,858E
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 971486
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 314-727-5188
 TELEFAX: 314-727-6092
 INFORMATION FOR SEQ ID NO: 201:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 291 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-931-858E-201

Query Match 61.4%; Score 289.4; DB 4; Length 291;
 Best Local Similarity 99.7%; Pred. No. 1; 5e-32;
 Matches 290; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 181 GCCCGTGTCTGTCATGGCAGGTGGCTGACCCGTGCGGAGCTAGGCCG 240
 Db 1 GCGCGTGTCTGTCATGGCAGGTGGCTGACCCGTGCGGAGCTAGGCCG 60
 Qy 241 GGCTAGCCCTCAGGGAGAGGTCACTTCCTCTACTGGCGCGGAAGTGGCTG 300
 Db 61 GGCTAGCCCTCAGGGAGAGGTCACTTCCTCTACTGGCGCGGAAGTGGCTG 120
 Qy 301 GCCCCCACCCAGATGGCTGGCTGGCCGGTCAAGGCCAGGGAGCCAGGT 360
 Db 121 GCCCCCACCCAGATGGCTGGCTGGCCGGTCAAGGCCAGGGAGCCAGGT 180
 Qy 361 GGGCGCTGTGGCTGGCCCACTCTACCGAGTGCCCTCTGATGACGCC 420
 Db 181 GGGCGCTGTGGCTGGCCCACTCTACCGAGTGCCCTCTGATGACGCC 240
 Qy 421 TGGCACGGCTGGCCAGCTCGGGCTGCTGGGGCTGGCTGGCTGGCTGA 471
 Db 241 TGGCACGGCTGGCCAGCTCGGGCTGCTGGGGCTGGCTGGCTGGCTGA 291

RESULT 8
 US-08-931-858E-202/c
 Sequence 202, Application US/08931858E
 Patent No. 622022

GENERAL INFORMATION:
 APPLICANT: MILBRANDT, JEFFREY D
 APPLICANT: KOTZBAUER, PAUL T
 APPLICANT: LAMPE, PATRICIA A
 APPLICANT: KLEIN, ROBERT
 APPLICANT: DESAUVAGE, FRED
 APPLICANT: HOWELL & HAERKAMP, L.C.
 NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESS:
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MO
 COUNTRY: USA
 ZIP: 63105

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/931,858E
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 971486
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 314-727-5188
 TELEFAX: 314-727-6092
 INFORMATION FOR SEQ ID NO: 202:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 291 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-931-858E-202

Query Match 61.4%; Score 289.4; DB 4; Length 291;
 Best Local Similarity 99.7%; Pred. No. 1; 5e-52;
 Matches 290; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 181 GCCCGTGTCTGTCATGGCAGGTGGCTGACCCGTGCGGAGCTAGGCCG 240
 Db 291 GCGCGTGTCTGTCATGGCAGGTGGCTGACCCGTGCGGAGCTAGGCCG 232
 Qy 241 GGCTAGCCCTCAGGGAGAGGTCACTTCCTCTACTGGCGCGGAAGTGGCTG 300
 Db 231 GGCTAGCCCTCAGGGAGAGGTCACTTCCTCTACTGGCGCGGAAGTGGCTG 172
 Qy 301 GCCCCCACCCAGATGGCTGGCTGGCCGGTCAAGGCCAGGGAGCCAGGT 360
 Db 171 GCCCCCACCCAGATGGCTGGCTGGCCGGTCAAGGCCAGGGAGCCAGGT 112
 Qy 361 GGGCGCTGTGGCTGGCCCACTCTACCGAGTGCCCTCTGATGACGCC 420
 Db 111 GGGCGCTGTGGCTGGCCCACTCTACCGAGTGCCCTCTGATGACGCC 52
 Qy 421 TGGCACGGCTGGCCAGCTCGGGCTGCTGGGGCTGGCTGGCTGGCTGA 471
 Db 51 TGGCACGGCTGGCCAGCTCGGGCTGCTGGGGCTGGCTGGCTGGCTGA 1

RESULT 9
 US-08-931-858E-222
 Sequence 222, Application US/08931858E
 Patent No. 622022

GENERAL INFORMATION:
 APPLICANT: JOHNSON, EUGENE M
 APPLICANT: MILBRANDT, JEFFREY D
 APPLICANT: KOTZBAUER, PAUL T
 APPLICANT: LAMPE, PATRICIA A
 APPLICANT: KLEIN, ROBERT
 APPLICANT: DESAUVAGE, FRED
 APPLICANT: HOWELL & HAERKAMP, L.C.
 NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESS:
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MO
 COUNTRY: USA
 ZIP: 63105

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/931,858E
 FILING DATE: 05-08-2003
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 971466
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 314-727-5188
 TELEFAX: 314-727-6092
 INFORMATION FOR SEQ ID NO: 222:
 SEQUENCE FOR SEQ ID NO: 222:
 LENGTH: 267 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 S-08-931-858E-222

Query Match	56.7%	Score 267
Best Local Similarity	100.0%	Pred. No.
Matches	267	Misma
Y	196 TCCCACTCTGGAGCTGACCCCTCCCTGGAA	
o	1 TCCCACTGTGAGCTGACCCCTCCCTGGCA	
Y	256 GAGAAGTCATCTTCGCTACTGGCCGGAGG	
o	61 GAGAAGTCATCTTCGCTACTGGCCGGAGG	
Y	316 GGCCTGGCTGCGCCGGCTGAGGCCAGGG	
o	121 GGCCTGGCTGCGCCGGCTGAGGCCAGGG	
Y	376 CCACCTGCTACACGAGCTGGCTTCCTGAT	
o	181 CCACCTGCTACACGAGCTGGCTTCCTGAT	
Y	436 CAGCTCTGGGGCTGCGCTGGCTGT 462	
o	241 CAGCTCTGGGGCTGCGCTGT 267	

RESULT 10
 S-08-931-858E-179
 Sequence No. 179, Application US/08/931858E
 Patent No. 622022
 GENERAL INFORMATION:
 APPLICANT: JOHNSON, EUGENE M.
 APPLICANT: MILLBRANDT, JEFFREY D.
 APPLICANT: KOBZAUER, PAUL T.
 APPLICANT: LAMPE, PATRICIA A.
 APPLICANT: KLEIN, ROBERT
 APPLICANT: DESAUVAGE, FRED
 TITLE OF INVENTION: PESEPHIN AND RELATED
 NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE
 CITY: ST. LOUIS
 STATE: MO
 COUNTRY: USA
 ZIP: 63105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version 1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/931,858E
 FILING DATE:
 CLASSIFICATION: 435

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/931,858E
 FILING DATE: 314-727-5188
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 971486
 TELECOMMUNICATION INFORMATION:
 LENGTH: 471 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-931-858E-180

SEQUENCE CHARACTERISTICS:
 LENGTH: 471 base pairs
 SEQUENCE FOR SEQ ID NO: 180:
 ATGGCGTAGGAAACTTCTGCTGGGCCTCTGCTGCTGCTGACCTGGGACAG 60
 Db 471 ATGCTCTCGAGAAAGACTTCGATTCGTGCTCGCTCGCCCTCGACCCCTC 412
 Qy 61 GCGGGCCCGATGGGATCCGGTGGCATGGAGACTCTCTGACAG 120
 Db 411 GGTTGGTCTTGTACCTAAGGCTTGTGGAGATAAGCTCTATGGAAAG 355
 Qy 121 GTCGAAAGGCTGGGGACTCTGGCTGGGCACCCACCG --GCCCTTGGCCGGCTGGC 177
 Db 354 ATGGAGAGACTAGGGACCTGGACCTGGACGCCATAGGGTAACACATGTCGTCTCCA 295
 Qy 178 CGAGCCCTGTCATGCCACTCGAGCTGGCCAGCTGGCAAGCTGGCTGGC 237
 Db 294 AGCGCTTGGCTGGCTGTCATCGAGCTGGCCAGCTGGCAACCTGGCTGAGCTGGC 235
 Qy 238 CGGGCTACGCTCTAGAGGAAGTCATCTCCGACTCTCCGACTGGCCGAGCTGGCCCTG 297
 Db 234 CTGGCTACGCTCTAGAGGAAGTCATCTCCGACTCTGGCTGGCAAGCTGGCCCTG 175
 Qy 298 GGTGGCGACCCACATGGCTCGGCTGGCCGGTGGAGGGAGGCCAC 357
 Db 174 GAGGCCGTCACCACTGTCAGCTGGCCGAGCTGGCTGGCTGGCTGGCTG 115
 Qy 358 GGTGGCGCCCTGGGGCCACTCTGGCTGGAGCTGGACCTGGCTGGACCCAC 417
 Db 114 GCGCACCCGCTGGCCACCACTGGCTGGAGCTGGCTGGCTGGCTGGCTGGCTGG 55
 Qy 418 CCTGGCAGGGCTCCAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGA 471
 Db 54 CATTGGCAGGCTCCAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGA 1
 Qy 912 GGTGGCGCCCTGGGGCCACTCTGGCTGGAGCTGGCTGGCTGGACCCAC 417
 Db 110 GCGCACCCGCTGGCCACCACTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 55
 Qy 418 CGCTGGCAGGGCTGGCCACCACTGGCTGGCTGGCTGGCTGGCTGGCTGA 471
 Db 418 CATGGCAGGCTCCAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGA 471
 RESULT 12
 US-08-931-858E-190
 Sequence 190, Application US/08/931,858E
 Patent No. 62,2022
 GENERAL INFORMATION:
 APPLICANT: JOHNSON, EUGENE M
 APPLICANT: MULBRANDT, JEFFREY D
 APPLICANT: KOPZBAUER, PAUL T
 APPLICANT: LAMPE, PATRICIA A
 APPLICANT: KLEIN, ROBERT
 DESAUVAGE, FRED

TITLE OF INVENTION: PERSPHIN AND RELATED GROWTH FACTOR
 NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS, MO
 STATE: MO
 COUNTRY: USA
 ZIP: 63105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/931,858E
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 971486
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 314-727-5188
 FAX: 314-727-6092
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 971486
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 314-727-5188
 FAX: 314-727-6092
 INFORMATION FOR SEQ ID NO: 190:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 471 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-931-858E-190

Query Match 53.1%; Score 250; DB 4; Length 471;
 Best Local Similarity 73.4%; Pred. No. 2.7e-44;
 Matches 348; Conservative 0; Mismatches 120; Indels 6; Gaps 2;

Qy 1 ATGGCGTAGGAAACTTCTGCTGGGCCTCTGCTGCTGACCTGGGACAG 60
 Db 471 ATGCTCTCGAGAAAGACTTCGATTCGTGCTCGCTCGCCCTCGACCCCTC 412
 Qy 61 GCGGGCCCGATGGGATCCGGTGGCATGGAGACTCTCTGACAG 120
 Db 411 GGTTGGTCTTGTACCTAAGGCTTGTGGAGATAAGCTCTATGGAAAG 355
 Qy 121 GTCGAAAGGCTGGGGACTCTGGCTGGGCACCCACCG --GCCCTTGGCCGGCTGGC 177
 Db 354 ATGGAGAGACTAGGGACCTGGACCTGGACGCCATAGGGTAACACATGTCGTCTCCA 295
 Qy 178 CGAGCCCTGTCATGCCACTCGAGCTGGCCAGCTGGCAAGCTGGCTGGC 237
 Db 294 AGCGCTTGGCTGGCTGTCATCGAGCTGGCCAGCTGGCAACCTGGCTGGC 235
 Qy 238 CGGGCTACGCTCTAGAGGAAGTCATCTCCGACTCTGGACTGGCCGAGCTGGCCCTG 297
 Db 234 CTGGCTACGCTCTAGAGGAAGTCATCTCCGACTCTGGCTGGCAAGCTGGCCCTG 175
 Qy 298 GGTGGCGACCCACATGGCTCGGCTGGCCGGTGGAGGGAGGCCAC 357
 Db 174 GAGGCCGTCACCACTGTCAGCTGGCTGGCTGGCTGGCTGGCTG 115
 Qy 358 GGTGGCGCCCTGGGGCCACTCTGGCTGGAGCTGGCTGGACCCAC 417
 Db 114 GCGCACCCGCTGGCCACCACTGGCTGGAGCTGGCTGGCTGGCTGGCTGG 55
 Qy 418 CCTGGCAGGGCTCCAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGA 471
 Db 54 CATTGGCAGGCTCCAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGA 1
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 Db 110 GCGCACCCGCTGGCCACCACTGGCTGGCTGGCTGGCTGGCTGGCTGG 55
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 RESULT 13
 US-08-931-858E-191/C

Sequence 191 Application US/089331858E
 Patent No. 6422022
 GENERAL INFORMATION:
 APPLICANT: JOHNSON, EUGENE M
 MILBRANDT, JEFFREY D
 APPLICANT: KOTZBAUER, PAUL T
 APPLICANT: LAMPE, PATRICIA A
 APPLICANT: KLEIN, ROBERT
 APPLICANT: DESAUTAGE, FRED
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
 NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MO
 COUNTRY: USA
 ZIP: 63105
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 APPLICATION NUMBER: US/08/931,858E
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 971486
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 314-727-5188
 TELEFAX: 314-727-6092
 INFORMATION FOR SEQ ID NO: 191:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 471 base pairs
 TYPE: Dna
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-931-058E-191

Query Match 53.1%; Score 250; DB 4; Length 471;
 Best Local Similarity 73.4%; Pred. No. 2 7e-44;
 Matches 348; Conservative 0; Mismatches 120; Indels 6; Gaps 2;

Qy 1 ATGGCGTGGCCCGATGCCGGTGGGGTCCCGGATGGAGACTTCGCTCTGAAACAG 60
 Db 471 ATGGCGTGGCCCGATGCCGGTGGGGTCCCGGATGGAGACTTCGCTCTGAAACAG 60
 Qy 61 GGCTGGGGCCCGATGCCGGTGGGGTCCCGGATGGAGACTTCGCTCTGAAACAG 120
 Db 411 GGCTGGGTCCCTGATCTTAAAGGGTCTGGCGGAT--GAGCTCTATCNGGAA 355
 Qy 121 GTGGCAAAGGCTGGGGACCTGGCTGGCCACCG--CCCGCTTGGCCGCTGGCC 177
 Db 354 ATGGCGAGACTGGAGGACTCATGGGATCAAAATGGCTGGAGCTGGCTGGCT 295
 Qy 178 CGAGGCTCTGCTGGCCATGGCCAGCTGGGAGGCTGGCTGGAGGCTAGGC 237
 Db 294 AGAGCTTACCTGGTTGTCGGCTGGCCGGTCAACAGTGGTGAAGCTGGC 235
 Qy 238 CTGGGCTACGCCCTAGAGGAAGGCTCATCTCCGCTACTCGGCCGCCCT 297
 Db 234 CTGGGCTATGCCCTAGAGGAAGGATATCTGGCTGAGCTGGAGCTGGCCCA 175
 Qy 298 GGTGGCGACCCAACTGGCTGGCCAGGGCGAGGGCCAGGCCAC 357
 Db 174 GAGGTCTGGTACCCACAGTCGGCTGGCCGGTCTCCAGGGAGGGTCAGCTCAT 115
 Qy 358 GGTGGCGACCCAACTGGCTGGCCAGGGCTGAGCTGGAGCTGGCCCAAC 417
 Db 114 GGAGACCTTGGCCAGCCCACAGCTATGCTGATGCTGACCTCTTGATGACCC 55
 Qy 418 CGTGGCACAGGGTGGCCAGCTGGCTGGCTGGCTGGCTGGCTGGCTGA 471
 Db 54 CATTGGCAGCAGCTGGCTCAAGCTGGCAGCTGGCTGGCTGGCTGGCTGA 1

RESULT 14
 US-08-981-739-175
 Sequence 175, Application US/08981739
 Patent No. 6232449
 GENERAL INFORMATION:
 APPLICANT: JOHNSON JR., EUGENE M.
 MILBRANDT, JEFFREY D.
 KOTZBAUER, PAUL T.
 LAMPE, PATRICIA A.
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
 NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: US
 ZIP: 63105-1817
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/981,739
 FILING DATE: 31-Aug-1988
 FILING DATE: 31-Aug-1988
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCW/US97/03461
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 CLASSIFICATION: <Unknown>
 PRIORITY DOCUMENT NUMBER: 976163
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314) 727-5188
 TELEFAX: (314) 727-6092
 INFORMATION FOR SEQ ID NO: 175:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 405 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 175:
 US-08-981-739-175

Query Match Similarity 44.1%; Score 207.6; DB 4;
 Best Local Similarity 79.4%; Pred. No. 1.9e-35;
 Matches 246; Conservative 0; Mismatches 64; Indels 9; Gaps 0;

Qy 162 CCTTCCTCCCTCGGCCAGGCCCTGCTGGCATTCCTAGCCAGTGGAGCTGACCTCTGC 221
 Db 96 CCATCTCGCTCTCAAGGCCCTGGCTGAGCTGGCTCATCCGACTGGCTACTGGCC 155
 Qy 222 CGTGGCAGAGCTAGGCCCTAGGCTCTAGGCCATGGAGAAGGTCTCCGCTACTGGCC 281
 Db 156 AGTGGCTGAGCTGGCCCTGGCTATGGCTGAGGAAGGTCTCCGATACTGGTC 215
 Qy 282 CGCGAGCTGCTGCCCTGGCTGGCTGCCAGCCAGCTGGCTGGCTGGCTGGCTGG 341
 Db 216 TGGCAGCTGCTCCAAAGGCCCTGGCTGAGCTGGCTACTGGCTGAGCTGG 275
 Qy 342 CCAGGGCGAGGCCACGCTGGCCCTGCTGGCTGAGCTGGCTACTGGCTGGCT 401
 Db 276 GCGGGTCGAGCCATGGCGACCTGCTGGCCACAGCTGGCTGAGCTGGACCTT 335

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2003, 11:32:18 ; Search time 313 Seconds
(without alignments)
3388.790 Million cell updates/sec

Title: US-09-220-617B-203

Perfect score: 471

Sequence: 1 ATGGCCCTAGGAAGTTCCT.....CCTCGGGCTGTTGGCTGA 471

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Sequences: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Post-processing: Minimum Match 0%, Maximum Match 100%
Listing first 45 summaries

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3: /SIDS2/gcdata/geneseg/genesegn-emb1/NA1982.DAT:*

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21: /SIDS2/gcdata/geneseg/genesegn-emb1/NA2000.DAT:*

22: /SIDS2/gcdata/geneseg/genesegn-emb1/NA2001A.DAT:*

23: /SIDS2/gcdata/geneseg/genesegn-emb1/NA2001B.DAT:*

24: /SIDS2/gcdata/geneseg/genesegn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	471	100.0	471	20 AAX60507	Human pre-pro pers
2	467.8	99.3	471	20 AAX60509	W09914235 Seq ID N
3	376	79.8	556	21 AA250334	Human Persephin-AR
c 4	5	343.4	72.9	556 21 AA250337	Human Persephin-AR
5	343	72.8	974	24 ABO44526	Human ovarian anti
6	332.4	70.6	974	22 AAFF7935	Human secreted pro
7	332.4	70.6	973	22 AAFF7903	DNA encoding novel
8	291.6	61.9	1173	23 AASPI1308	Human persephin pr
9	291	61.8	291	20 AAX60503	

ALIGNMENTS

RESULT 1	AAX60507	ID AAX60507 standard; cDNA; 471 BP.
XX	XX	Human pre-pro persephin cDNA sequence.
XX	XX	Growth factor; GF; persephin; neuron growth; cellular degeneration; peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke; Alzheimer's disease; Parkinson's disease; Huntington's disease; trauma; brain injury; spinal cord injury; nervous system tumour; infection; multiple sclerosis; cardiac muscle degeneration; injury; neurotoxin; metabolic disease; diabetes; renal dysfunction; neurulin; ss.
XX	XX	Homo sapiens.
XX	XX	W09914235-A1.
XX	XX	25-MAR-1999.
XX	XX	15-SEP-1998; 98W0-US19163.
XX	XX	16-SEP-1997; 97US-0931858.
XX	XX	(UNIW) UNIV WASHINGTON.
PI	PI	Desauvage F, Johnson EM, Klein R, Kotzbauer PT;
XX	XX	Lampe PA, Milbrandt JD;
XX	XX	

DR WPI; 1999-244023/20.
 DR P-PSDB; AAY16727.
 XX PT New isolated persenphin growth factor nucleic acids used to, e.g.
 XX PT promote neuronal growth
 XX PS Claim 19a, Page 199; 222pp; English.
 CC The invention relates to a novel isolated and purified growth factor (GF) that comprises persenphin or a fragment or a conservatively substituted variant. The persenphin GF polypeptides can promote the survival and growth of neurons and non-neuronal cells. The persenphin GF polypeptides or polynucleotides can be used for preventing or treating cellular degeneration or insufficiency, e.g., neuronal degeneration resulting from peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, acute spinal cord injury, nervous system tumours, acute brain injury, hematopoietic cell degeneration or multiple sclerosis, or infection, anaemias, thrombocytopenia, or insufficiency resulting from eosinopenia, anaemias, thrombocytopenia, or stem cell insufficiencies cardiac muscle degeneration or insufficiency resulting from cardiomyopathy or congestive heart failure. They can also be used for treating e.g. peripheral nerve trauma or injury, exposure to neurotoxins, metabolic diseases such as diabetes or renal dysfunctions and damage caused by infectious agents. The GF can also be used for promoting the growth and/or differentiation of a cell in a culture medium. The antisense polynucleotides can be used for treating a disease condition mediated by expression of persenphin by a population of cells.
 XX SQ Sequence 471 BP: 55 A: 170 C: 164 G: 82 T: 0 other;
 Query Match 100.0%; Score 471; DB 20; Length 471;
 Best Local Similarity 100.0%; Pred. No. 2.4e-86;
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGGCGTAGGAAAGTTCCTGGGTCTCTGCTCTGGCTCTGGTCAGCTGGAGAC 60
 Db 1 ATGGCGTAGGGAGTCCTGGCTCTGGCTCTGGCTCTGGCTCTGGAGCTGGACAG 60
 Qy 61 GGCGGGCCCATGGCGCTGGTCCCTGGCGATGGAGTCTGCTGAAAG 120
 Db 61 GGCGGGCCCATGGCGCTGGTCCCTGGCGATGGAGTCTGCTGAAAG 120
 Qy 121 GTGGAAAGCTGGAGGACCGGACCCACGGCCCCCTGGCGCCCTGGCGGA 180
 Db 121 GTGGAAAGCTGGAGGACCGGACCCACGGCCCCCTGGCGCCCTGGCGGA 180
 Qy 181 GCGCGTCGGTCTGGTCATGGCAAGCTGGCTGGCGCTGGCGAGCTGGCTG 240
 Db 181 GCGCTGTCGGTCTGGTCATGGCAAGCTGGCTGGCGCTGGCGAGCTGGCTG 240
 Qy 241 GGCTACGCTCTAGAGGAAAGTCATCTTCGGCTACTGGCCGGCAAGTGGCGCTGGCGAGCTGGCTG 300
 Db 241 GGCTACGCTCTAGAGGAAAGTCATCTTCGGCTACTGGCCGGCAAGTGGCGCTGGCGAGCTGGCTG 300
 Qy 301 GCGCGCACCCAGGATGGCTGGCGCTGGCGAGGGCGAGCCACGG 360
 Db 301 GCGCGCACCCAGGATGGCTGGCGCTGGCGAGGGCGAGCCACGG 360
 Qy 361 GGGCGCTGTCGGGGCCACCTGCTACAGCTGCTGGCGCTGGCGAGCCACGG 420
 Db 361 GGGCGCTGTCGGGGCCACCTGCTACAGCTGCTGGCGCTGGCGAGCCACGG 420
 Qy 421 TGGCAGGCGCTGGCCAGCTCGGGGGCTGGCTGCTGGCTGGCTGA 471
 Db 421 TGGCAGGCGCTGGCCAGCTCGGGGGCTGGCTGCTGGCTGGCTGA 471

XX DT 17-AUG-1999 (first entry)
 XX DE WO994235 Seq ID No: 205.
 XX Growth factor; GF; persenphin; neuron growth; cellular degeneration; peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke; Alzheimer's disease; Parkinson's disease; Huntington's disease; trauma; brain injury; spinal cord injury; nervous system tumour; infection; multiple sclerosis; cardiac muscle degeneration; injury; neurotoxin; metabolic disease; diabetes; renal dysfunction; neuritin; SB.
 XX Unidentified.
 XX CS
 XX PN WO994235-A1.
 XX PD 25-MAR-1999.
 XX PF 15-SEP-1998; 98RC-US19163.
 XX PR 16-SEP-1997; 97US-0931858.
 XX PA (UNIN) UNIV WASHINGTON.
 XX PI Desauvage F, Johnson EM, Klein R, Kotzbauer PT;
 PI Lampe PA, Milbrandt JD;
 XX DR 1999-244023/20.
 XX PA New isolated persenphin growth factor nucleic acids used to, e.g.
 PT Promote neuronal growth
 PT Promote neuronal growth
 XX PS Claim 19a; Page 200; 222pp; English.
 CC The invention relates to a novel isolated and purified growth factor (GF) that comprises persenphin or a fragment or a conservatively substituted variant. The persenphin GF polypeptides can promote the survival and growth of neurons and non-neuronal cells. The persenphin GF polypeptides or polynucleotides can be used for preventing or treating cellular degeneration or insufficiency, e.g., neuronal degeneration resulting from peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, acute spinal cord injury, nervous system tumours, acute brain injury, acute brain injury, acute spinal cord injury, metabolic diseases such as diabetes or renal dysfunctions and damage caused by infectious agents. The GF can also be used for promoting the growth and/or differentiation of a cell in a culture medium. The antisense polynucleotides can be used for treating a disease condition mediated by expression of persenphin by a population of cells. The products can also be used for detection and diagnosis.
 XX DR 1 ATGGCGTAGGAAAGTTCCTGGGTCTCTGCTCTGGCTCTGGTCAGCTGGAGAC 60
 CC 1 ATGGCGTAGGGAGTCCTGGCTCTGGCTCTGGCTCTGGAGCTGGACAG 60
 CC 61 GGCGGGCCCATGGCGCTGGTCCCTGGCGATGGAGTCTGCTGAAAG 120
 CC 61 GGCGGGCCCATGGCGCTGGTCCCTGGCGATGGAGTCTGCTGAAAG 120
 CC 121 GTGGAAAGCTGGAGGACCGGACCCACGGCCCCCTGGCGCCCTGGCGGA 180
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 CC 181 GCGCGCACCCAGGATGGCTGGCGCTGGCGAGGGCGAGCCACGG 360
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 CC 361 GGGCGCTGTCGGGGCCACCTGCTACAGCTGCTGGCGCTGGCGAGCCACGG 420
 CC 361 GGGCGCTGTCGGGGCCACCTGCTACAGCTGCTGGCGCTGGCGAGCCACGG 420
 CC 421 TGGCAGGCGCTGGCCAGCTCGGGGGCTGGCTGCTGGCTGA 471
 CC 421 TGGCAGGCGCTGGCCAGCTCGGGGGCTGGCTGCTGGCTGA 471

XX SQ Sequence 471 BP: 55 A: 172 C: 164 G: 80 T: 0 other;
 Query Match 99.3%; Score 467.8; DB 20; Length 471;
 Best Local Similarity 99.6%; Pred. No. 1.1e-85;
 Matches 469; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 ATGGCGTAGGAAAGTTCCTGGGTCTCTGCTCTGGCTCTGGTCAGCTGGAGAC 60
 Db 1 ATGGCGTAGGGAGTCCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGTCAGCTGGAGAC 60
 Qy 61 GGCGGGCCCATGGCGCTGGTCCCTGGCGATGGAGTCTGCTGAAAG 120
 Db 61 GGCGGGCCCATGGCGCTGGTCCCTGGCGATGGAGTCTGCTGAAAG 120
 Qy 121 GTGGAAAGCTGGAGGACCGGACCCACGGCCCCCTGGCGCCCTGGCGGA 180
 Db 121 GTGGAAAGCTGGAGGACCGGACCCACGGCCCCCTGGCGCCCTGGCGGA 180

RESULT 2
 AAX60509 ID AAX60509 Standard; cDNA: 471 BP.
 XX AC AAX60509

CC immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immuno-deficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome, Chaga's cardiomopathy and coronary arteriosclerosis), angiogenic disorders (e.g. corneal graft, neovascularisation and diabetic retinopathy), neurological disorders (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis. The nucleic acid molecules may be used to produce the secreted polypeptides. They may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples. The polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators of their expression and activity.

50 Sequence 974 BP; 179 A: 297 C: 329 G: 165 T: 4 other:

Query Match 72.8%; Score 343; DB 22; Length 974;
Best Local Similarity 82.9%; Pred. No. 1.6e-60;
Matches 461; Conservative 3; Mismatches 4; Indels 8B; Gaps 3;

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218 ATGGCCGTAGGAAAGTTCCTGCTGGCTCTGTCAGTGGACAG 277

Qy 61 GGCCTGGCCCGGATGCCGCGGGTTCCTGTGCTGACAG 120

Db 278 GGCTGGGGCCCGGATGCCGCGGGTTCCTGTGCTGACAG 337

Qy 121 GTGGCAAAGGCTGGAGGGACCTGGCTG----- 147

Db 338 GTGGCAAAGGCTGGAGGGACCTGGCTG----- 397

Qy 148 ----- 155

Db 398 CAACTTCCCCACCCCTGACCTGCTACTGTGAGCCCTGCTGACAG 457

Qy 156 CCCCTCCCTTGGCCCGTGGCCGAGCCCTGCTGCTGAGCTGTGAC 215

Db 458 CCCCTCCCTTGGCCCGTGGCCGAGCCCTGCTGAGCTGTGAC 517

Qy 216 CCGTGGCTGGAGACCTAGCCCTGGCTGACGCTCACTTGGCTA 275

Db 518 CCGTGGCTGGAGACCTAGCCCTGGCTGACGCTCACTTGGCTA 577

Qy 276 CTGGCGGGGCACTGCCCGCTGGCCGACCCAGATGGCTGGCGGCCGCT 335

Db 578 CTGGCGGGCACTGCCCGCTGGCCGACCCAGATGGCTGGCGGCCGCT 637

Qy 336 GCAGGGCCAGGCCGAGCCACGGTGGGGCCCACTGGCTACCCAGT 395

Db 638 GCAGGGCCAGGCCGAGCCACGGTGGGGCCCACTGGCTACCCAGT 697

Qy 396 GGCTCTCTGGTGAACGGCCACGGTGGGGCTGGCTGGCTGGCTGCTG 455

Db 698 GGCTCTCTGGTGAACGGCCACGGTGGGGCTGGCTGGCTGGCTGCTG 754

Qy 456 CGCTGTGTGTGTG 471

Db 755 CGCTGTGTGTG 770

Qy 770 CGCTGTGTGTG 770

Db 770 CGCTGTGTGTG 770

Qy 794 CGCTGTGTGTG 770

Db 816 CGCTGTGTGTG 770

Qy 838 CGCTGTGTGTG 770

Db 860 CGCTGTGTGTG 770

Qy 882 CGCTGTGTGTG 770

Db 904 CGCTGTGTGTG 770

Qy 926 CGCTGTGTGTG 770

Db 950 CGCTGTGTGTG 770

Qy 974 CGCTGTGTGTG 770

Db 992 CGCTGTGTGTG 770

KW dermatological; antiinflammatory; anti-HIV; cytostatic; cardiotonic;
KW vascular; anti-angiogenic; opthalmological; neuroprotectant;
KW nootropic; anticonvulsant; anti-Alzheimer's; anti-parkinsonian;
KW antimicrobial; pulmonary; vaccine; gene therapy; cancer;
KW protein coordinate data; infection; SB.
XX Homo sapiens.

OS XX

PN XX

PD XX

PI XX

PI XX

PI XX

WPI 2001-235311/24.

XX

PT XX

PT XX

PT XX

PT XX

PS XX

KW dermatological; antiinflammatory; anti-HIV; cytostatic; cardiotonic;
KW vascular; anti-angiogenic; opthalmological; neuroprotectant;
KW nootropic; anticonvulsant; anti-Alzheimer's; anti-parkinsonian;
KW antimicrobial; pulmonary; vaccine; gene therapy; cancer;
KW protein coordinate data; infection; SB.
XX Homo sapiens.

OS XX

PN XX

PD XX

PI XX

PI XX

PI XX

WPI 2000WO-US26013.

XX

PT XX

KW dermatological; antiinflammatory; anti-HIV; cytostatic; cardiotonic;
KW vascular; anti-angiogenic; opthalmological; neuroprotectant;
KW nootropic; anticonvulsant; anti-Alzheimer's; anti-parkinsonian;
KW antimicrobial; pulmonary; vaccine; gene therapy; cancer;
KW protein coordinate data; infection; SB.

XX

PN

PD

PI

PI

PI

WPI

XX

PT

KW dermatological; antiinflammatory; anti-HIV; cytostatic; cardiotonic;
KW vascular; anti-angiogenic; opthalmological; neuroprotectant;
KW nootropic; anticonvulsant; anti-Alzheimer's; anti-parkinsonian;
KW antimicrobial; pulmonary; vaccine; gene therapy; cancer;
KW protein coordinate data; infection; SB.

XX

PN

PD

PI

PI

PI

WPI

XX

PT

216	CCGTCCGGTGGCAAGCTAGGCTTACGCCCTGGCTTACGCCCTAGGGAGAAGGTCATCTTCGGCTA	275
518	CTCTGCCCTGGCAAGCTAGGCTTACGCCCTAGCTCATAGGAA -GTCATCTTCGGCTA	576
276	CTGGCCGGCAGGTGGCCCGTGGCTGGCCCGACCCAGATGGCCATGGCTGGGGCTGGCCGGCT	335
577	CTGGCCGGCAGGTGGCCCGTGGCCCGTGGCTGGCCCGACCCAGATGGCCATGGCTGGGGCTGGCCGGCT	636
336	GCAGGGCCAGGGCGAGCCCAAGGTGGGCCCTGCTGGCCGCCATGGCTAGCCAGCTGGCTAGCCAGT	395
637	GCAGGGCCAGGGCGARCCCAAGGGCGCTGGCCCACTGGCTACCCACGT	696
396	GGCTCTCTCGATGACGGCCACGCCCTGGCAAGCGCTGCCCACTCTGGGGCTGCCCTG	455
697	GGCTCTCTCGACGGCCCACTGGCTGCCCACTCTGGGGCTGCCCACTCTGGGGCT -CTG	753
456	CGGCTGTTGGTGCCTGA 471	
754	CGGCTGTTGGTGCCTGA	769
SULT 8		
AAS81308 standard; cDNA; 1173 BP.		
AAS81308;		
13-FEB-2002 (first entry)		
DNA encoding novel human diagnostic protein #17112.		
Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.		

Claim 15: Page 196; 224pp; English.

The invention relates to a novel isolated and purified growth factor (GF) that comprises persenphin or a fragment or a conservatively substituted variant. The persenphin GF polypeptides can promote the survival and growth of neurons and non-neuronal cells. The persenphin GF polypeptides or polynucleotides can be used for preventing or treating cellular degeneration or insufficiency, e.g. neuronal degeneration resulting from peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, ischaemic stroke, acute brain injury, acute spinal cord injury, nervous system trauma, multiple sclerosis, or infection, hematopoietic cell degeneration or insufficiency resulting from eosinopenia, anemias, thrombocytopoenia, or stem cell insufficiencies, cardiac muscle degeneration or insufficiency resulting from cardiomopathy or congestive heart failure. They can also be used for treating e.g. peripheral nerve trauma or injury, exposure to neurotoxins, metabolic diseases such as diabetes or renal dysfunctions and damage caused by infectious agents. The GF can also be used for promoting the growth and/or differentiation of a cell in a culture medium. The antisense polynucleotides can be used for treating a disease condition mediated by expression of persenphin by a population of cells. The products can also be used for detection and diagnosis.

RESULT 10
AAX60505
ID AAX60505 standard; CDNA; 291 BP.

AC AAX60505;
XX 17-AUG-1999 /first entry\

human persephin protein encoding cDNA.

Homo sapiens
W09914235-A1.

W09914235 seq ID No: 190

CC	disease, Parkinson's disease	XX	Sequence 291	BP;	33	A;	112	C
CC	acute brain injury, acute sp	SG	Query Match	61.48				
CC	multiple sclerosis, or infec		Best Local Similarity	99.78				
CC	insufficiency resulting from		Matches 290;	Conservative				
CC	stem-cell insufficiencies, ca							
CC	resulting from cardionyopath							
CC	be used for treating e.g. pe							
CC	neurotoxins, metabolic disea							
CC	and damage caused by infecti							
CC	promoting the growth and/or							
CC	medium. The antisense polynu							
CC	condition mediated by expres							
CC	The products can also be used							
XX								
SG								
Qy	181	GGCTGTGTCAGTCATGCCAGCT						
Db	1	GCCCTGTCAGTCATGCCAGCT						
Qy	241	GGCTAGGCTCAAGGGAAAGT						
Db	61	GGCTAGGCTCAAGGGAAAGT						
Qy	301	GCCCCACCCAGATGGCTGCC						
Db	121	GCCCCACCCAGATGGCTGCC						
Qy	361	GGCCCTGCTGGCCCACTCG						
Db	181	GGCCCTGCTGGCCCACTCG						
Qy	421	TGGCAGCCTGGCTGCCAGCTC						
Db	241	TGGCAGCCTGGCTGCCAGCTC						

112 AAX6049 / Standard: CINA; 4/1 DF.
XX AC AAX60497;
XX

XX DF W09914235 seq ID No: 190

15-SEP-1998; 98WO-US19163.
 16-SEP-1997; 97US-0931858.

(UNIV) UNIV WASHINGTON.

PI Desaive F, Johnson EM, Klein R, Kotzbauer PT;
 Lampe PA, Milbrandt JD;
 XX XX XX XX

WPI: 1999-24403/20.

New isolated persephin growth factor nucleic acids used to, e.g.
 promote neuronal growth

Claim 15; Page 199; 222pp; English.

CC The invention relates to a novel isolated and purified growth factor (GF)
 CC that comprises persephin or a fragment or a conservatively substituted
 CC variant. The persephin GF polypeptides can promote the survival and
 CC growth of neurons and non-neuronal cells. The persephin GF polypeptides
 CC or polynucleotides can be used for preventing or treating cellular
 CC degeneration or insufficiency, e.g. neuronal degeneration resulting from

Sequence 291						
Match		Score		Length		
Query	Match	Best Local Similarity	Score	DB	20:	291:
Qy	181	61.4%	289.4	DB 20:	Length 291;	
Dbb	1	99.7%	Pred. No. 1e-49;			
Qy	181	61.4%	289.4	DB 20:	Length 291;	
Dbb	1	99.7%	Pred. No. 1e-49;			
Qy	1	Conservative	0;	Mismatches	1;	Indels 0;
Qy	241	61.4%	289.4	DB 20:	Length 291;	
Dbb	1	99.7%	Pred. No. 1e-49;			
Qy	241	61.4%	289.4	DB 20:	Length 291;	
Dbb	1	99.7%	Pred. No. 1e-49;			
Qy	61	61.4%	289.4	DB 20:	Length 291;	
Dbb	1	99.7%	Pred. No. 1e-49;			
Qy	301	61.4%	289.4	DB 20:	Length 291;	
Dbb	121	61.4%	289.4	DB 20:	Length 291;	
Qy	361	61.4%	289.4	DB 20:	Length 291;	
Dbb	181	61.4%	289.4	DB 20:	Length 291;	
Qy	421	61.4%	289.4	DB 20:	Length 291;	
Dbb	241	61.4%	289.4	DB 20:	Length 291;	

AAA60497; Scenario: C1N1; 4/1 DF.
XXX
AC
XXX

W09914235 Sea ID No: 190

Growth factor; GF; persephin; neuron growth; cellular degeneration; Peripheral neuropathy; amyotrophic lateral sclerosis; ischaemic stroke; Alzheimer's disease; Parkinson's disease; Huntington's disease; trauma; brain injury; spinal cord injury; nervous system tumour; infection; metabolic disease; cardiac muscle degeneration; injury; neurotoxin; metabolic disease; diabetes; renal dysfunction; neuritin; ss.

Db	336	CTCTGATGTCAGCACCATTGGAGCAGCTCAGCTCTAGTGAGCTTGCTG	395
Qy	462	TGGTGGCTGA	471
Db	396	TGGTGGCTGA	405

unintended.
WO9914235-A1.
25-MAR-1999.
15-SEP-1998; 98WO-US19163.
16-SEP-1997; 97US-0931858.
(UNIW) UNIV WASHINGTON.
Desaive F, Johnson EM, Klein R, Kotzbauer PT;
Lampe PA, Milbrandt JD;
WPI; 1999-244023/20.
New isolated persephin growth factor nucleic acids used to, e.g.
promote neuronal growth

Disclosure: Page 188: 222pp; English.

The invention relates to a novel isolated and purified growth factor (GF) that comprises persenitin or a fragment or a conservatively substituted variant. The persenitin GF polypeptides can promote the survival and growth of neurons and non-neuronal cells. The persenitin GF polypeptides or polynucleotides can be used for preventing or treating cellular degeneration or insufficiency, e.g. neuronal degeneration resulting from peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, Huntington's disease, ischemic stroke, acute brain injury, acute spinal cord injury, nervous system tumours, multiple sclerosis, or infection, hematopoietic cell degeneration or insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or stem-cell insufficiencies, cardiac muscle degeneration or insufficiency resulting from cardiomyopathy or congestive heart failure. They can also be used for treating e.g., peripheral nerve trauma or injury, exposure to neurotoxins, metabolic diseases such as diabetes or renal dysfunctions and damage caused by infectious agents. The GF can also be used for promoting the growth and/or differentiation of a cell in a culture medium. The antisense polynucleotides can be used for treating a disease condition mediated by expression of persenitin by a population of cells. The products can also be used for detection and diagnosis.

6

Qy	162	CCATGGCCGCGCTGGCGAGCCCTGCTGGTCCATGCCAGCTGGAGCCCTGACCCGTC	221
Db	120	CCATGGCTGCTCCAGAGCTTGCTGGCTACGCCACTGGGCCACTGGCCCTACCCATCC	179
Qy	222	CGGGCAGAGCTAGGGCTGGCTACGCCCTAGAGGAGGCTACTCTCCGCTACTCGGC	281
Db	180	AGTGGCTAGCTGGGGCTGGCTATGCCCTGGAGAGGTACATCCTGGATACGTGCG	239
Qy	282	CGGAGCTGGCCGGCTGGCCGAGCCAGCCATGGCCCTGGCCGCTGGCCGCTGGAGG	341
Db	240	TGGCACTGGTCCCAGGGCCGPNACCCAGCACGTCAGTCAGTCAGTCAGTCAGG	299
Qy	342	CCAGGGCAGGCCACGCTGGCCCTGCGCCACTCGTACACCGAGCTGGCTT	401
Db	300	GCGGGGTGGAGGCCATGGCCGACCCCTGGCCGCTGGCCAGCAGCTGGACCTT	359
Qy	402	CCATGATGCCGCAACGGCTGGAGGGTGGCCCAAGCTCGGGAGCTGGCTG	461
Db	360	CCATGATGATGCCGACCCATTGGCAGGCTGGCTCAGCTCAGCTCAGCTGAGCTG	419
Qy	462	TGGTGGCTGA	471
Db	420	TGGTGGCTGA	429

Search completed: March 7, 2003, 11:44:13
 Job time : 316 secs


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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TIMAGE: 3104342"
/clone.lib="NCI_CGAP_Sub9"
/tissue_type="mixed"
/dev_stage="mixed"
/lab.host="DH10B (Life Technologies)"
/note="Vector: pTR73-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoR I; Site_2: Not I; tissues:
Colonic mucosa with Crohns disease, Colonic mucosa with
ulcerative colitis, Fetal thymus, Cervix, Cervical
adenosquamous carcinoma, Ligament cells, Prostate,
carcinoma, Bladder carcinoma, Brain oligodendroga;
NCI_CGAP_Sub9 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-800, 1996. First strand cDNA synthesis was prime
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pTR73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library sequence tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are CGTC, AACG, GGGCC,
GGAAC, TACG, TAAGC, ATGGC, ATCAC. For additional
information, contact: Bento Soares, bento-soares@uowa.edu
TAG LIB-DT-H-COO
TAG TISSUE=colonic mucosa with Crohns disease
NASE COUNT
TAG SEQ=CGTC"
TAG_a_165_c_178_g_89_t

```

RESULT 2	HW050617/c	ORGANISM	Homo sapiens
LOCUS	AM050617	DEFINITION	W21901.x1 Soares_Dieckgraef_NHCD Homo sapiens cDNA clone IMAGE:2558497 3' similar to SW:RTN_HUMAN Q93748 NEUROTURIN PRECURSOR: ; mRNA sequence.
ACCESSION		VERSION	AM050617
KEYWORDS		EST	AM050617.1 GI:5912887
SOURCE		human.	

REFERENCE	FEATURES	SOURCES	BASE COUNT	QUERY MATCHES	RESULT
AUTHORS			ORIGIN	Best Locus	BM665236/
TITLE				Matches	LOCUS
JOURNAL					DEFINITION
COMMENT					ACCESSION

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

ON nucleic - nucleic search, using sw model
Run on: March 7, 2003, 11:33:49 ; Search time 2567 Seconds
(without alignments)
5339.860 Million cell updates/sec

Title: US-09-220-617B-203
Perfect score: 471
Sequence: 1 ATGCCCTAGGGAAAGTCTCT.....CCCTGGGGTGTGGTGGCTGA 471

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank:
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2: 9b_hhg:*

3: 9b_in:*

4: 9b_on:*

5: 9b_ov:*

6: 9b_pc:*

7: 9b_ph:*

8: 9b_pk:*

9: 9b_pr:*

10: 9b_ro:*

11: 9b_sts:*

12: 9b_sy:*

13: 9b_ua:*

14: 9b_v1:*

15: em_ba:*

16: em_fun:*

17: em_jum:*

18: em_ln:*

19: em_miu:*

20: em_cm:*

21: em_cr:*

22: em_cv:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_y1:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htg_hum:*

40: em_htg_mus:*

41: em_htg_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	471	100.0	471	9 AF040962	AF040962 Homo sapi
2	372.8	79.2	2180	9 AK055490	AK055490 Homo sapi
3	372.8	79.2	116819	9 AC011491	AC011491 Homo sapi
c	4	250	53.1	471 10 AF040960	AF040960 Mus muscu
	5	250	53.1	471 10 AF040961	AF040961 Rattus no
	6	207.6	44.1	405 6 ARI52134	ARI52134 Sequence
	7	207.6	44.1	544 6 ARI52107	ARI52107 Sequence
	8	207.6	44.1	559 6 ARI52120	ARI52120 Sequence
	9	206	43.7	213137 10 AC073683	AC073683 Mus muscu
	10	203	43.1	559 6 ARI52121	ARI52121 Sequence
c	11	199.2	43.1	142758 2 ARI12629	ARI12629 Rattus no
	12	199.8	42.4	291 6 ARI152133	ARI152133 Sequence
	13	195	41.4	291 6 ARI152135	ARI152135 Sequence
	14	189.6	40.3	391 6 ARI152109	ARI152109 Sequence
	15	186.6	39.6	273 6 ARI152100	ARI152100 Sequence
	16	180.6	38.3	267 6 ARI152098	ARI152098 Sequence
	17	180.6	38.3	267 6 ARI152099	ARI152099 Sequence
	18	148.8	31.6	336 6 ARI152104	ARI152104 Sequence
	19	148.8	31.6	336 6 ARI152108	ARI152108 Sequence
	20	79.8	16.9	306 6 ARI001492	ARI001492 Sequence
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	24	79.8	16.9	306 6 ARI152050	ARI152050 Sequence
	25	79.8	16.9	425 6 ARI001505	ARI001505 Sequence
	26	79.8	16.9	425 6 ARI005241	ARI005241 Sequence
	27	79.8	16.9	425 6 ARI044793	ARI044793 Sequence
	28	79.8	16.9	425 6 ARI062999	ARI062999 Sequence
	29	79.8	16.9	425 6 ARI152063	ARI152063 Sequence
	30	79.8	16.9	591 6 ARI001494	ARI001494 Sequence
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	34	79.8	16.9	591 6 ARI152052	ARI152052 Sequence
	35	79.8	16.9	594 9 HS778110	U78110 Human pr
	36	79.8	16.9	1160 9 HS862618	AL16195 Human pr
	37	79.8	16.9	80893 9 AC024592	AC024592 Homo sapi
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c	39	78.2	16.6	169893 2 AC021165	AC021165 Homo sapi
c	40	69.2	14.7	675 6 AX410388	AX410388 Sequence
	41	69.2	14.7	675 10 AF109402	AF109402 Mus muscu
	42	69.2	14.7	190446 2 AL627128	AL627128 Mus muscu
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	44	67.2	14.3	663 6 AX055740	AX055740 Sequence
	45	67.2	14.3	663 6 AX01382	AX01382 Sequence

ALIGNMENTS

RESULT	1	LOCUS	AF040962	DEFINITION	Hom sapiens persephin mRNA	ACCESSION	AF040962	VERSION	GI: 2935709	ORGANISM	Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominidae; Homo.
											1 (bases 1 to 471)
											Milbrandt, J., de Sauvage, F.J., Farhner, T.J., Baloh, R.H.,
											Leitner, M.L., Tansey, M.G., Lampe, P.A., Heucher, R.O., Kotzbauer, P.T., Simburg, K.S., Golden, J.P., Davies, J.A.,
											Pred. No. is the number of results predicted by chance to have a

Vejsada, R., Kato, A.C., Hynes, M., Sherman, D., Nishimura, M., Wang, L.-C., Vandlen, R., Moffat, B., Klein, R.D., Poulsen, K., Garces, A., Henderson, C.E., Phillips, H.S. and Johnson, M.M.,	Persephin, a novel neurotrophic factor related to GDNF and neurotulin	Neuron 20 (2), 245-253 (1998)	2 (bases 1 to 471)	oligo capping; <i>fis</i> (full insert sequence). Homo sapiens fetus brain cDNA to mRNA, clone_111: FEBRA2	
REFERENCE	de Sauvage, F.J., Klein, R.D., Fahrner, T.J. and Milbradt, J.	Direct Submission	1	KEYWORDS SOURCE	
AUTHORS	Submitted (05-JAN-1998) Pathology, Washington University Medical School, 660 S. Euclid Ave., St. Louis, MO 63110, USA	JOURNAL	1	ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. Homo sapiens	
FEATURES	Location/Qualifiers	source	1	REFERENCE AUTHORS	
	1. 471 /organism="Homo sapiens" /db_xref="Taxon:9606" 1. .471 /note="neurotrophic factor; PSP" /codon_start=1 /product="persephin" /protein_id="AC3940.1" /db_xref="GI:23957210" /translation="MAVGFLGLSLLISLQLQGMPDARGVPADGEFSESEQVAK GCTWLGHTRPLARLRLSOPCQMSLTSVAVLGLYASEKVKVTRYCGSCPRGAR TQHGLALARLOGOGRAHGGCFCRTRYDVAFLDDRURWQLPQLSAAACGCGG"	REFERENCE 2 (bases 1 to 2180) Isogai, T., Otaku, T. and Sugiyama, T.	1	REFERENCE AUTHORS	
CDS		JOURNAL	1	REFERENCE TITLE	
		Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 15332-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp). Tel: 81-438-52-3955, Fax: 81-438-52-3986	JOURNAL	1	REFERENCE TITLE
		COMMENT	1	COMMENT	
			1	COMMENT	
BASE COUNT	55 a 170 c 164 g 82 t	ORIGIN	1	COMMENT	
ORIGIN			1	COMMENT	
Query Match	100.0%	Score 471; DB 9; Length 471;	1	COMMENT	
Best Local Similarity	100.0%	Pred. No. 3e-71; 0: Indels 0: Gaps 0;	1	COMMENT	
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Db	1 ATGGCGTAGGGAGTTCTCTGCTGGCTCTGCMCTCTGTCAGCTGGACAG 60	1 ATGCCGTAGGGAGTTCTCTGCTGGCTCTGCMCTCTGTCAGCTGGACAG 60	1	COMMENT	
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Db	181 GCCGTCTGCTGCTCATGGCAGCTGTCAGCTGGCTGACCTGTCGCGCAGAGCTTGGCTG 240	181 GCCGTCTGCTGCTCATGGCAGCTGTCAGCTGGCTGACCTGTCGCGCAGAGCTTGGCTG 240	1	COMMENT	
Qy	241 GGCTAGGCTCAGAGGAGGTCATCTCCCTACTGGCGGGAGCTGTCGCTGGCTG 300	241 GGCTAGGCTCAGAGGAGGTCATCTCCCTACTGGCGGGAGCTGTCGCTGGCTG 300	1	COMMENT	
Db	241 GGCTAGGCTCAGAGGAGGTCATCTCCCTACTGGCGGGAGCTGTCGCTGGCTG 300	241 GGCTAGGCTCAGAGGAGGTCATCTCCCTACTGGCGGGAGCTGTCGCTGGCTG 300	1	COMMENT	
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Qy	361 GCGCCCTGCTGCCGCTGGCTGGCTGCCCTCTGCGGCCAGCCACCGC 420	361 GCGCCCTGCTGCCGCTGGCTGGCTGCCCTCTGCGGCCAGCCACCGC 420	1	COMMENT	
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Qy	421 TGGCAAGGGCTGCCAGCTGGCTGGCTGCCCTCTGCGGCCAGCCACCGC 471	421 TGGCAAGGGCTGCCAGCTGGCTGGCTGCCCTCTGCGGCCAGCCACCGC 471	1	COMMENT	
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RESULT	2		1	COMMENT	
AK055490	AK055490		1	COMMENT	
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DEFINITION				PRI 01-AUG-2002	
				clone FEBRA2006793, weakly similar	
ACCESSION	AK055490			to PERSEPHIN PRECURSOR.	
VERSION	AK055490.1			GI:16550224	

Query	Best Local Similarity	Local	Score	Length	Match	Source
QY 336 GCAGGGCAGGGCCAGGCCACGGTGGCCCTGCTGCGCCCACTCGCTAACCCACGT 395	84.4%	Pred.	No. 5.5-55;			
QY 1899 GCAGGGCAGGGCCACGGTGGCCCTGCTGCGCCCACTCGCTAACCCACGT 1958	Conservative	0;	Mismatches	2;	Indels	85;
QY 396 GGCCCTTCCTCTGATGACCCACGGCTGGCAGGGCTCGCCACTGCTAACCCACGT 455	Matches	469;	Conservative		Gaps	1;
Db 1959 GGCCCTTCCTGATGACCCACGGCTGGCAGGGCTCGCCACTGCTAACCCACGT 2018	1	ATGGCGTAGGGAGTTCTGCTGGGTCTCTGCTGGCTCTGCTGGAGCTGGGAG 60	QY			
QY 456 CGCTGTGGTGGTGA 471	Db 77366 ATGGCGTAGGGAGTTCTGCTGGGTCTCTGCTGGCTCTGCTGGAGCTGGGAG 77307					
Db 2019 CGGCTGTGGTGGTGA 2034	QY 61 GGCTGGCCGATGCCGTGGTGGTGGTGGCTGGCTGGAGACTCTGCTGA 120					
RESULT 3 AC011491/c	Db 77306 GGCTGGCCGATGCCGTGGTGGCTGGAGACTCTGCTGA 77247					
LOCUS AC011491	QY 121 GTGCCAAAGCTGGACCTGGCTGTAAGGACTTCAAGGACCTGGCTG 147					
DEFINITION Homo sapiens chromosome 19 clone CTB180A7, complete sequence.	Db 77246 GTGCCAAAGCTGGACCTGGCTGTAAGGACTTCAAGGACCTGGCTG 77187					
ACCESSION AC011491	QY 148 -----					
VERSION GI:15281206	Db 77186 CAACTTTCCCAGCCCTAACCTGCTGCTACCTGTCAGGCCCTCCACAGGCC 155					
KEYWORDS	Db 77126 CGGCCCTGTCGCCGCCAGCTGGCTGGCTAGCCCTAGGCCCTGGCTG 77127					
ORGANISM Homo sapiens	QY 156 CGCCGCCCTGCGCCCTGCGCCAGCTGGCTCATGCCAGCTGGAGCC 215					
REFERENCE 1 (bases 1 to 118819)	Db 77126 CGGCCCTGTCGCCGCCAGCTGGCTGGCTAGCCCTAGGCCCTGGCT 77067					
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.	QY 216 CCTGTCCGTTGGCAGAGCTGGCTGGCTCATGCCAGCTGGAGCTGGCTA 275					
JOURNAL Direct Submission	Db 77066 CCTGTCCGTTGGCAGAGCTGGCTGGCTAGCCCTAGGCCCTGGCT 77007					
REFERENCE 2 (bases 1 to 118819)	QY 276 CTGGCCGGCGAGCTGGCCCGACCCAGCATGGCTGGCCCTGGCCGGCT 335					
AUTHORS DOE Joint Genome Institute.	Db 77006 CTGGCCGGCGAGCTGGCCCGACCCAGCATGGCTGGCCCTGGCCGGCT 76947					
JOURNAL Direct Submission	QY 336 GCAGGGCAGGGCCAGGCCACGGTGGCCCTGCTGCCCTGACCTGCTACCCACGT 395					
REFERENCE 3 (bases 1 to 118819)	Db 76946 GCAGGGCAGGGCCAGGCCACGGGGCGACTGCTGCCCTGACCCACGT 76887					
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.	QY 396 GGCCCTTCCTGAGAACCCCCACCGCTGACGGTGGCCCTGGCTGGCTGGCT 455					
JOURNAL Direct Submission (23-OCT-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA	Db 76886 GGCCCTTCCTGAGAACCCCCACCGCTGACGGTGGCCCTGGCTGGCTGGCT 76827					
REFERENCE 4 (bases 1 to 118819)	QY 456 CGGTGTTGGTGTGA 471					
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.	Db 76826 CGGTGTTGGTGTGA 76811					
JOURNAL Direct Submission (23-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA	RESULT 4 AF040960					
COMMENT On Aug 23, 2001 this sequence version replaced gi:10947022.	LOCUS AF040960					
Draft Sequence Produced by DOE Joint Genome Institute	DEFINITION 471 bp mRNA					
www.jgi.doe.gov	ACCESSION AF040960					
Finishing Completed at Stanford Human Genome Center	VERSION AF040960.1					
www-singl.stanford.edu	KEYWORDS					
Quality: Phrap Quality >=40 99.9% of Sequence:	ORGANISM					
Estimated Total Number of Errors is 0.	Mus musculus					
STS Content:	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus					
SHGC-31644 G28545	REFERENCE 1 (bases 1 to 471)					
SHGC-35441 G28816	AUTHORS Milbradt, J., de Sauvage, F. J., Fahrner, T. J., Baloh, R. H., Leitner, M. L., Tansey, M. G., Lampe, P. A., Heuckeroth, R. O., Kotzbauer, P. T., Simburger, K. S., Golden, J. P., Davies, J. A., Vejsada, R., Kato, A. C., Hynes, M., Sherman, D. P., Nishimura, M., Wang, L. -C., Vanderson, R., Moffat, B., Klein, R. D., Poulsen, K., Garces, A., Henderson, C. E., Phillips, H. S., and Johnson, E. M.					
Note: at basepair 20107	TITLE Persephin, a novel neurotrophic factor related to GDNF and					
there is a discrepancy between the plasmid library and the original	JOURNAL Neuron 20 (2), 245-253 (1998)					
M13 shotgun lib. The following sequence is the consensus according	MEDLINE 98105050					
to the M13 clones:	PUBLMED 949196					
tgacaggtaacggccgtctctactaaaaataaaaaataggccggcatggccggccgc	REFERENCE 2 (bases 1 to 471)					
ctgtatcccaatcgggaggctgtaaatcgaggatgggtgtatccggaggccggatgtgcgt	AUTHORS Fahrner, T. J., Heuckeroth, R. O., Simburger, K. S., Kotzbauer, P. T., and Milbradt, J.					
gaccc. Location/Qualifiers	JOURNAL Direct Submission (05-JAN-1998) Pathology, Washington University Medical School, St. Louis, MO 63110, USA					
1..118819	Submitted (05-JAN-1998)					
/organism="Homo sapiens"	Source					
/db_xref="taxon:9606"						
/chromosome="19"						
/clone="C1B-180A7"						
BASE COUNT 29880 a 29980 c 30977 g 27982 t	Query Match 79.2% Score 372.8; DB 9; Length 118819;					
ORIGIN	JOURNAL					

REFERENCE 1 (bases 1 to 405) Unclassified.
 AUTHORS Johnson, E. M., Jr., Milbrandt, J. D., Kotzbauer, P.T. and Lampe, P.A.
 TITLE Persenphin and related growth factors
 JOURNAL Patent: US 6222449-A 175 15-MAY-2001;
 FEATURES Location/Qualifiers 1...405
 source /organism="unknown"
 BASE COUNT 71 a 132 c 108 g
 ORIGIN

Query Match 44.1%; Score 207.6; DB 6; Length 405;
 Best Local Similarity 79.4%; Pred. No. 3.8e-26;
 Matches 246; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
 Qy 162 CCTGCCGCGCTGCGCGAGCCCTATGCCATGGCTGAGCCCTGTC 221
 Db 96 CCATGTCGCTTCAGACCTTGGCTGTCATGGCAGCTGGACCTTACCC 155
 Qy 222 CTGGCGAGCTAGGCCCTGGCTACGGAGAAAGTCATCTTCGCTACTGGC 281
 Db 156 AGTGGCTGAGCTGGCTGGCTAGCCCTGGAGAGGTCACTTCGCTATGGC 215
 Qy 282 CGCAGCTGCCCTGGCTGCCAACCCAGCATGGCTGGCGCTGGCGCTAGGG 341
 Db 216 TGGAGGTGCCCCAACAGAGCTTACCCAGCACGNTGGTACGGCTGGAGG 275
 Qy 342 CCAGGCGAGCCCAACGGCTGGCCCACTGGCTAGCCACGTCGGCTT 401
 Db 276 CGGGTCGACCCCTGGCGACCTGGCCACCCAGCTGATGTCACCTT 335
 Qy 402 CCTCGATGACGCCAACCGCTGGCGCCGCTGGCTGGCGCTGGCTGGCTG 461
 Db 336 CCTTGATGATGACGCCAACATGGCACAGCTGGCTCACTCAGGGCAAGCTGGCTG 395
 Qy 462 TGGGGCTGA 471
 Db 396 TGGGGCTGA 405

RESULT 7 AR152107
 LOCUS Sequence 105 from patent US 6232449.
 DEFINITION Sequence 105 from patent US 6232449.
 VERSION AR152107
 KEYWORDS Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 544) Unclassified.
 AUTHORS Johnson, E. M., Jr., Milbrandt, J. D., Kotzbauer, P.T. and Lampe, P.A.
 TITLE Persenphin and related growth factors
 JOURNAL Patent: US 6232449-A 105 15-MAY-2001;
 FEATURES Location/Qualifiers 1...544
 source /organism="unknown"
 BASE COUNT 115 a 158 c 153 g 118 t
 ORIGIN

Query Match 44.1%; Score 207.6; DB 6; Length 544;
 Best Local Similarity 79.4%; Pred. No. 3.5e-26;
 Matches 246; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
 Qy 162 CCTGCCGCGCTGGCTGCCAGCTGGCTCATGGCAGCTGGAGCTGACCTGTC 221
 Db 120 CCATGTCGCTTCAGACCTGGCTCATGGCTGTCATGGCAGCTGGAGCTGACCTGTC 179
 Qy 222 CGTGGCGAGCTAGGCCCTGGCTACAGGAGAAAGTCATCTTCGGCTACTGGC 281
 Db 180 AGTGGCTGACCTGGCCCTGGCTAGGAGAAAGTCATOTTCGATACTGTC 239
 Qy 282 CGGACGCTGCCCTGGCTGCCAGCTGGCTGCCAGCTGGCTGCCAGCTGGCTG 341

REFERENCE 1 (bases 1 to 405) Unclassified.
 AUTHORS Johnson, E. M., Jr., Milbrandt, J. D., Kotzbauer, P.T. and Lampe, P.A.
 TITLE Persenphin and related growth factors
 JOURNAL Patent: US 6222449-A 175 15-MAY-2001;
 FEATURES Location/Qualifiers 1...405
 source /organism="unknown"
 BASE COUNT 71 a 132 c 108 g
 ORIGIN

Query Match 44.1%; Score 207.6; DB 6; Length 405;
 Best Local Similarity 79.4%; Pred. No. 3.8e-26;
 Matches 246; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
 Qy 162 CCTGCCGCGCTGGCTGCCAGCTGGCTCATGGCAGCTGGAGCTGACCTGTC 221
 Db 240 TGGCAGCTGTCCTCAAGAGGCCCTACCCAGCACAGCTGGTACTGGCCGGCTGAG 299
 Qy 342 CCAGGCGAGCCACGGCTGGCCCTGGCTGCGGCTACCTACCCGAGCTGGCCCT 401
 Db 300 GCGGGTCGACCCATGGCAGCCCTGGCTGAGCTGGCTGACCTGTCATGGTACCT 359
 Qy 402 CCTCGATGACGCCAACCGCTGGCGCCGCTGGCTGGCTGCCAGCTGGGGCTGCTGGCTG 461
 Db 360 CCTTGATGATGACGCCAACATGGCACAGCTGGCTCATGGCAGCTGGCTG 419

RESULT 8 AR152120
 LOCUS AR152120 559 bp DNA
 DEFINITION Sequence 131 from patent US 6232449.
 VERSION AR152120
 KEYWORDS Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 559)
 AUTHORS Johnson, E. M., Jr., Milbrandt, J. D., Kotzbauer, P.T. and Lampe, P.A.
 TITLE Persenphin and related growth factors
 JOURNAL Patent: US 6232449-A 131 15-MAY-2001;
 FEATURES Location/Qualifiers 1...559
 source /organism="unknown"
 BASE COUNT 100 a 173 c 155 g 131 t
 ORIGIN

Query Match 44.1%; Score 207.6; DB 6; Length 559;
 Best Local Similarity 79.4%; Pred. No. 3.5e-26;
 Matches 246; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 162 CCTTGCCGCTGGCCGAGCCCTGGCTGCGGCTACCTGGCTGAGCTGGCTG 221
 Db 250 CCATGTCGCTTCAGCCAGCTGGCTGGCTGCTGTCATGGCAGCTGGCTGACCTGAC 309
 Qy 222 CGTGGAGACTGACCTGGCTGGCTGAGCTGGCTGAGAGTCATCTTCGGCTACTGGC 281
 Db 310 AGTGGCTGACCTGGCCCTGGCTGATGCTCGAAGAGTCATTTGGCTGAGATGGSC 369
 Qy 282 CGGAGCTGCCCTGGCTGGCTGCCAGCATGGCTGGCTGGCTGGCTGGCTGGCTGAG 341
 Db 370 TGGCAGCTGTCCTCCAAAGGGCCCTAACCGAGCACAGTCGGTACTGGCCCTGGCTGAG 429
 Qy 342 CCAGGCGAGCCACGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGAG 401
 Db 430 GCGGGTCGAGCCATGGCAGCCCTGGCTGAGCTGGCTGGCTGGCTGGCTGGCTGAG 489
 Qy 402 CCTCGATGACGCCAACCGCTGGCGCCGCTGGCTGGCTGCCAGCTGGCTGAGCTGGCTG 461
 Db 490 CCTTGATGATGACGCCAACATGGAGCACCTGGCTGAGCTGGCTGGCTGGCTG 549

RESULT 9 AC073683
 LOCUS AC073683 213137 bp DNA
 DEFINITION Mus musculus chromosome 17 clone RP23-124G7, complete sequence.
 VERSION AC073683
 FEATURES AC073683...3 GI:20043100
 KEYWORDS HTG...
 SOURCE Mus musculus.

ORGANISM	Mus musculus		Db	8366	TGGTGGCTGA	8375
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;						
Metazoa; Mollusca; Insecta; Arthropoda; Nematoda; Chordata; Mammalia; Muridae; Murinae; Mus .						
REFERENCE	1 (bases 1 to 213137)		RESULT	10		
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center .		AR152121	AR152121	559 bp	DNA
TITLE	Direct Submission		LOCUS	AR152121	Sequence 134 from patent US 6232449.	
JOURNAL	UNpublished		DEFINITION	AR152121		
REFERENCE	2 (bases 1 to 213137)		ACCESSION	AR152121		
AUTHORS	DOE Joint Genome Institute .		VERSION	AR152121.1		
TITLE	Direct Submission		KEYWORDS	GI:15118171		
JOURNAL	Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		ORGANISM	Unknown.		
REFERENCE	3 (bases 1 to 213137)		SOURCE	Unknown.		
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center .		UNCLASSIFIED	Unclassified.		
TITLE	Direct Submission		REFERENCE	1 (bases 1 to 559)		
JOURNAL	Submitted (20-APR-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		AUTHORS	Johnson,E.M.Jr., Milbrandt,J.D., Kotzbauer,P.T. and Lampe,P.A.		
REFERENCE	4 (bases 1 to 213137)		TITLE	Persephin and related growth factors		
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center .		JOURNAL	US 6232449-A 134 15-MAY-2001;		
TITLE	Direct Submission		FEATURES	Location/Qualifiers		
JOURNAL	Submitted (26-FEB-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		source	1..559		
REFERENCE	5 (bases 1 to 213137)		BASE COUNT	104 a	/organism="unknown"	
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center .		ORIGIN	166 C	150 g	139 t
TITLE	Direct Submission		QUERY MATCH	43.1%	Score 203;	DB 6;
JOURNAL	Submitted (05-APR-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		Best Local Similarity	78.8%	Pred. No. 2.1e-25;	Length 559;
REFERENCE	6 (bases 1 to 213137)		Matches	242	Conservative	0; Mismatches 65; Indels 0; Gaps 0;
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center .		QY	165	TGCCTGGCTGCGAGCCCTCTCTCCATGCAAGCTGGACCTGACCTGCGGT	224
TITLE	Direct Submission		Db	253	TGTCGGCTTCAGAGCTTACCTGGCTTGTGGGGCTTGAGGCTGACCTCTACCACT	312
JOURNAL	Submitted (16-APR-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		QY	225	GGAGAGCTAGGCTGGCTAGGCCTAGGAGAGGTCATCTTCGCGTACTGCGGG	284
COMMENT	On Apr 5, 2002 this sequence version replaced 91:18767417.		Db	313	GGCTGAGCTGGCTGGCCATGCGCTGAGGAGAGATACTCCGATACTGCGT	372
AUTHORS	Draft Sequence Produced by DOE Joint Genome Institute		QY	285	CAGCTGCCCGCTGGCTGGCCACCCAGCTGGCTGGCCCTGCGCTGAGGGCA	344
TITLE	Finishing Completed at Stanford Human Genome Center		Db	373	CAGCTGCCCCAGAGGTCTGACCCAGACAGTGGCTGGCCCTGTTGGGGCA	432
JOURNAL	www-shoc.stanford.edu		QY	345	GGCGGAGGCCAGGTGGCCCTGCGCCACCTGGCTGAGCTGCGCTTCT	404
COMMENT	/chromosome="17"		Db	433	GGCTGAGCTGAGACCTGTGCACTGGCTGGCCACAGTATGGTGTATGCTCCT	492
AUTHORS	Estimated Total Number of Errors is 1.2.		QY	405	CGATGACCCCAACGCCAGGGCTGGCAGGGCTGGCTGGCTGGCTGG	464
TITLE	Location/Qualifiers		Db	493	TGATGACCCACCAATTGGCGAGCTGAGCTGCGCTAGCTGCGCTGG	552
JOURNAL	1..213137		QY	465	TGGCTGA	471
REFERENCE	/organism="Mus musculus"		Best Local Similarity	79.0%	Pred. No. 1.7e-16;	
AUTHORS	/db_xref="Taxon:10090"		Matches	245;	Conservative 0; Mismatches 65; Indels 0; Gaps 0;	
TITLE	/chromosome="17"		Db	553	TGGCTGA	559
JOURNAL	/clone="RP3-124G7"		BASE COUNT	52043	a	52259 g
COMMENT	56272 t		ORIGIN			
FEATURES			Query Match	43.7%	Score 206;	DB 10;
SOURCE			Best Local Similarity	79.0%	Pred. No. 1.7e-16;	Length 213137;
ORIGIN			Matches	245;	Conservative 0; Mismatches 65; Indels 0; Gaps 0;	
Db	8066	CCATGTCGCTTCAGAGCTTGGCTGAGCTGACCTTAC	RESULT	11	AC129629/c	
Qy	222	CGTGCAGAGCTAGGCCATGGCCATGGCTAGGAAAGGCTCATCTCCGGTACTGGC	LOCUS		AC129629	
Db	8126	AGTGGCTGAGCTGGCTGGCCGGCTATGCCAGGAAAGSTCTCGATCTG	DEFINITION		Rattus norvegicus clone CH230-11715, *** SEQUENCING IN PROGRESS	
Qy	282	CGGAGCTGCCGTGGCCGCCAGGATGCCCTGGCTGGCGCTGGAGGG	ACCESSION		**,* 74 unordered pieces.	
Db	8186	TGGCAGCTGGCTCCAAAGGGCCATACCCAGGCTATGGTACTGGC	VERSION		AC129629	
Qy	342	CCAGGCCAGGCCAACGGCCACTCGCTACCGACCTGGCTGGCC	KEYWORDS		HTC; RMGS; PHASE1.	
Db	8246	GGGGGGTCGACCTGGCCATGGCGACCTGCTGGAGCCACAGCTATGGTACTGG	ORGANISM		Rattus norvegicus	
Qy	402	CCTCGATGACGCCACCCGGTGGCGGCTGCCAGCTCGGGGCTCCGGCT	SOURCE		Eukaryota; Metasoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Db	8306	CCTTGATGATGACGCCATGGCAGACCTGCTCAGTGGCA	REFERENCE		Rattus norvegicus	
Qy	462	TGGTGGCTGA	AUTHORS		Rattus	
					1 (bases 1 to 142758)	
					Allen,C., Metzger,M., Lee., Abramzon,S., Adams,C., Alder,J.,	
					Allen,H., Alstrooks,S., Amin,A., Angelino,D.,	
					Ayalepechi,V., Aoyagi,A., Ayodele,I.M., Baca,E., Baden,H.,	
					Baranahane,D., Barber,M., Barnstead,M., Benahmed,F.,	
					Baldwin,D., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,	
					Biswalo,K., Buhay,C., Burch,P., Burrell,K., Calderon,E.,	
					Bryant,N., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,	

Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacon, J., Chavez, D., Chen, G., Chen, Z., Chen, Y., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Benson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Egan, A., Escott, M., Eugens, C., Evans, C.A., Fallis, T., Fan, G., Fernandez, S., Finley, N., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabis, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebrgeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Herrende, J., Hernandez, R., Hines, S., Hladun, H., Hodge, A., Hogen, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Joliver, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovari, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Liu, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longpere, S., Lopez, J., Lorenshewa, L., Louised, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, J., Mangum, A., Mangan, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhliney, S., Mcleod, M., Mcneill, T., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundada, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokeleme, O., Okunolu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puaio, M., Quirio, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruit, S.J., Sanders, W., Savery, G., Scheer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajis, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, P., Williams, G., Wilson, R., Wieczyk, R., Woeden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yaku, S., Yen, J., Yoon, L., Yoon, Y., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhäusern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G., and Gibbs, R.A.

TITLE **JOURNAL** **AUTHORS** **TITLE**
 Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE **AUTHORS** **TITLE**
 Submitted (24-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT **JOURNAL** **AUTHORS** **TITLE**
 Unpublished Direct Submission **2** (bases 1 to 142758)
 Workley, K.C.

JOURNAL **AUTHORS** **TITLE**
 Direct Submission **2** (bases 1 to 142758)

JOURNAL **AUTHORS** **TITLE**
 Contact: <http://www.hgsc.bcm.tmc.edu/>

REFERENCE **AUTHORS** **TITLE**
 Center Project name: GYMO
 Center Clone name: CH230-1171J15
 Center Summary: Summary Statistics
 Sequencing vector: Plasmid
 Chemistry: Dye-terminator Big Dye: 1008 of reads
 Assembly program: Phrap; version 0.99039
 Consensus quality: 63896 bases at least Q40
 Consensus quality: 69324 bases at least Q30
 Consensus quality: 73620 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank/draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 74 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1051:	contig of 1051 bp in length
1151:	gap of unknown length
1152:	contig of 1271 bp in length
2422:	gap of unknown length
2523:	contig of 1243 bp in length
3765:	gap of unknown length
3766:	gap of unknown length
4876:	contig of 1011 bp in length
4877:	gap of unknown length
5421:	contig of 1445 bp in length
6531:	gap of unknown length
6532:	contig of 1045 bp in length
7566:	gap of unknown length
7567:	gap of unknown length
7666:	gap of unknown length
8114:	contig of 1048 bp in length
8814:	gap of unknown length
8815:	contig of 1178 bp in length
9992:	gap of unknown length
9993:	contig of 1178 bp in length
10092:	gap of unknown length
11121:	contig of 1629 bp in length
11722:	gap of unknown length
12916:	contig of 1095 bp in length
12917:	gap of unknown length
13017:	contig of 1052 bp in length
14068:	contig of 1052 bp in length
14069:	gap of unknown length
14168:	gap of unknown length
15291:	contig of 1123 bp in length
15292:	gap of unknown length
16534:	contig of 1143 bp in length
16634:	gap of unknown length
16635:	contig of 1249 bp in length
17883:	gap of unknown length
17884:	contig of 1071 bp in length
17984:	contig of 1071 bp in length
19054:	gap of unknown length
19154:	contig of 1424 bp in length
20588:	contig of 1434 bp in length
20589:	gap of unknown length
21775:	contig of 1087 bp in length
21875:	gap of unknown length
22977:	contig of 1102 bp in length
23077:	gap of unknown length
24103:	contig of 1026 bp in length
24104:	gap of unknown length
24204:	contig of 1012 bp in length
25216:	gap of unknown length
25316:	contig of 1049 bp in length
26665:	gap of unknown length
27655:	contig of 1191 bp in length
27755:	gap of unknown length
27756:	contig of 16662 bp in length
29417:	gap of unknown length
29517:	gap of unknown length
34265:	contig of 1173 bp in length
35438:	contig of 1623 bp in length
35439:	gap of unknown length
35539:	contig of 1427 bp in length
31241:	contig of 1030 bp in length
32270:	gap of unknown length
32370:	gap of unknown length
34165:	contig of 1123 bp in length
38189:	gap of unknown length
38288:	contig of 1111 bp in length
38289:	contig of 1173 bp in length
39499:	gap of unknown length
39500:	contig of 1594 bp in length
41094:	gap of unknown length
42376:	contig of 1183 bp in length
42377:	gap of unknown length

RESULT 14									
QY	361	GGCCCTGCTGGGCCACTCGTACACCGACTTCTCGATGCCAACCGC	420						
Db	181	AGACPTGCTCCAGCCACCACTATGCTGATGCCAACCAT	240						
QY	421	TGGAGGGGCCCCAGCTCGGGCTGGCTGGCTGA	471						
Db	241	TGGAGGGGCCCCAGCTCGGGCTGGCTGGCTGA	291						
ORIGIN									
QY	256	GAGAAGTCATCTCGCTACTGGCCGAGTGCCCTGGCCACAGAT	315						
Db	61	GAGAAGATATCTCGAFACTGTGCACTGTCAGCTGCCAACGAC	120						
QY	316	GGCTGGCTGGAGCTGGCCGGTGAAGGGCCACGGCC	375						
Db	121	AGCTGGCTGGCCGGTGAAGGGCCACGGCC	180						
REFERENCE									
AUTHORS	Johnson, E. M., Jr., Milbradt, J. D., Kotzbauer, P. T. and Lampe, P. A.								
TITLE	Persephin and related growth factors								
JOURNAL	Patent: US 6232449-A 10-15-MAY-2001;								
FEATURES	Location/Qualifiers								
SOURCE	1. .391								
BASE COUNT	84 a	106 c	117 g	84 t					
ORIGIN									
QY	40	Query Match 40.3%; Score 189.6; DB 6; Length 391;							
Db	222	Best Local Similarity 80.4%; Pred. No. 4.6e-23; Matches 222; Conservative 0; Mismatches 54; Indels 0; Gaps 0;							
QY	196	TGCCACCTGAGGCTGACCTTGCCCTGGAGAAGTGAACCTGGCTAGCCAGAG	255						
Db	1	TGCCGCTGAGGCTGACCTTGCCCTGGAGAAGTGAACCTGGCTAGCCAGAG	60						
QY	256	GAGAAGTCATCTCGCTACTGGCCGAGCTGGCTGGCTGGCCACCCAGAT	315						
Db	61	GAGAAGATTATCTCGAFACTGTGCACTGTCAGCTGCCAACGAC	120						
QY	316	GGCTGGCTGGAGGCTGGAGGCTGGAGGCTGGCTGGCCCG	375						
Db	121	AGCTGGCTGGCCGGTGAAGGGCCACGGCC	180						
QY	376	CCACTCGCTACACGACTGGCTGATGCCAACGGCCACCGCTGGCTGCC	435						
Db	181	CCACCAAGCTGATGTGACTTCTGATGCCAACGGCCACCGCTGGCTGCC	240						
QY	436	CAGCTCTGGGGTGCCTGGCTGGCTGGCTGGCTGGCT	471						
Db	241	CAGCTCTAGCCGAGCTGTGGCTGGCTGCC	276						
RESULT 15									
AR152100	AR152100	Sequence 86 from patent US 6232449.	273 bp	DNA	Linear	PAT 08-AUG-2001			
LOCUS									
DEFINITION									
ACCESSION	AR152100								
VERSION	AR152100.1								
KEYWORDS									
SOURCE									
ORGANISM									
REFERENCE	1 (bases 1 to 273)								
AUTHORS	Johnson, E. M., Jr., Milbradt, J. D., Kotzbauer, P. T. and Lampe, P. A.								
TITLE	Persephin and related growth factors								
JOURNAL	Patent: US 6232449-A 10-15-MAY-2001;								
FEATURES	Location/Qualifiers								
SOURCE	1. .273								
BASE COUNT	45 a	85 c	82 g	61 t					

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